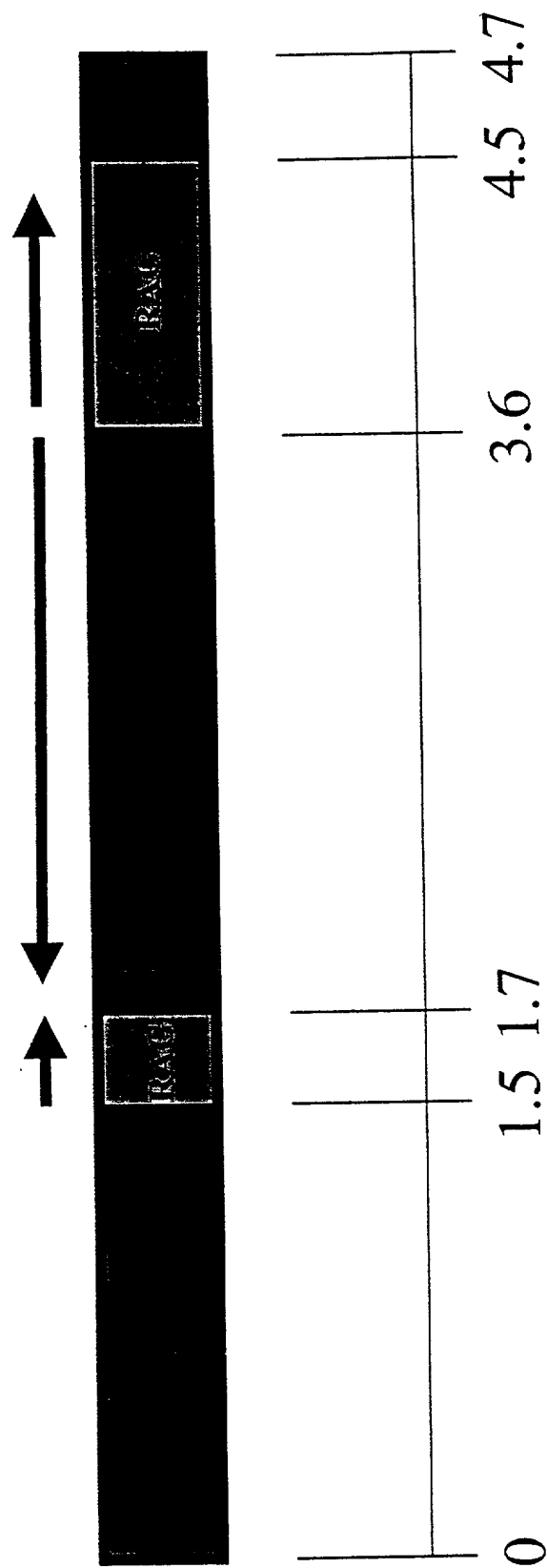


Figure 1. BOVINE RAG2 SEQUENCE

>
>
> 773 ATGTCACT ACAGATGGTA ACAGTCGGAA
>
> 801 ATAGCATAGC CTTAATTCAA CCAGGCTTCT CGTTAATGAA
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>
> 851 CAAGTTTTCT TCTTTGGCCA AAAAGGCTGG CCCAAGAGGT
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>
> 901 TGGAGTTTTC CATTTTGAGG TAAAGCATAA TCATCTTAAA
CTGAAGCCTG
>
> 951 CAGTTTTCTC TAAGGATTCC TGCTACCTTC CTCCTCTTCG ATACCGGGC
>
> 1001 CACTTGCACA TTCAGCGGCC AACTTGGAGT CTGAAAAGCA
TCAGTACATC
>
> 1051 ATCCATGGAG GAAAAACACC AAACAATGAG CTTTCAGATA
AGATTTATGT
>
> 1101 GATGTCTGTT GTTTCCAAGA ACAACAAAAA AGTTACCTTT
CGCTGCACAG
>
> 1151 AGAAGGACTT GGTAGGAGAC ATTCCTGAAG GCAGATATGG
TCATTCCATT
>
> 1201 GATGTGGTGT ATAGTCGGGG GAAAAGTATG GGTGTTCTCT
TTGGAGGACG
>
> 1251 GTCATACATA CTTTCTGCCC AAAGAACCAC AGAGAAATGG
AACAGTGTAG
>
> 1301 CTGACTGCCT GCCCCATGTC TTCTTGGTGG ATTTTGAATT
TGGGTGCTCT
>
> 1351 ACGTCATACA TTCTTCCAGA ACTTCAAGAT GGACTATCTT
TTCATGTCTC
>
> 1401 CATTGCCAGA AATGATACCG TTTATATTTT AGGAGGCCAT
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> 1451 ATAACATCCG CCCTGCCAAT CTGTACAGAA TAAGGGTTGA
TCTCCCCCTG
>

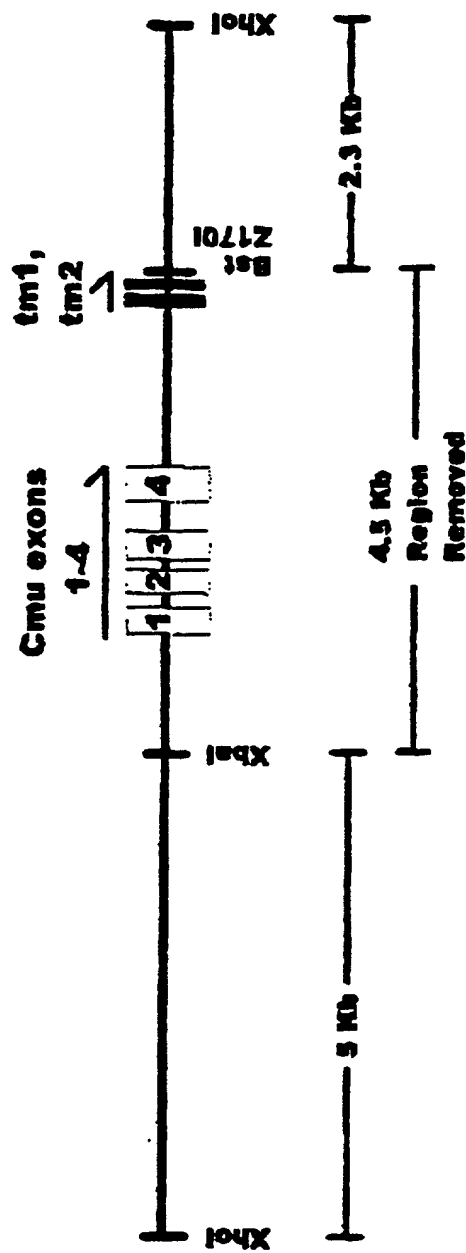
> 1501 GGTAGCCCAG CTGTGGAGTG CACAGTCTTG CCAGGAGGAA
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>
> 1551 CAGTGCAATC CTGACTCAAA TAAGCAATGA TGAATTTGTT
ATTGTTGGTG
>
> 1601 GCTATCAGCT TGAAAATCAA AAAAGAATGG TCTGTAACAT
CATCTCTTTC
>
> 1651 AAGTATAACA AGATAGACAT TCTTGAGATG GAAACCCCAG
ATTGGACCCC
>
> 1701 AGATATTAAG CACAGCAAGA TATGGTTTGG AAGCAACATG
GGAAATGGAA
>
> 1751 CTGTTTTCTC CGGCATACCA GGAGACAATA AACAGGCTGT
TTCAGAAGCA
>
> 1801 TTTTACTTCT ATACATTGAA ATGTGCTGAA GACGATGTGA
ACGAAGATCA
>
> 1851 GATAACTTTG ACAAGTAGTC AGACATCAAC AGAAGACCCA
GGGGACTCCA
>
> 1901 CTCCCTTTGA AGACTCAGAA GAATTTTGCT TCAGCGCAGA
AGCAAACAGT
>
> 1951 TTCGATGGTG ATGATGAATT TGACACCTAC AATGAAGATG
ATGAGGAAGA
>
> 2001 TGAGTCTGAG ACAGGCTATT GGATTACATG CTGCCCTACT
TGTGATGTGG
>
> 2051 ATATCAATAC GTGGGTACCA TTTTATTCAA CTGAGCTCAA
CAAGCCTGCC
>
> 2101 ATGATCTATT GCTCTCATGG AGATGGACAT TGGGTCCATG
CCCAGTGTAT
>
> 2151 GGATCTGGCA GAACGCACCA CCTCATCCAT CTATCAGAAG
GAAGCAATAA
>
> 2201 ATATTAYTGT AACGAGCATG TGGAGATAG

FIG. 2 - MAP OF BOVINE RAG-2 KNOCKOUT CONSTRUCT



→ = TRANSCRIPTIONAL ORIENTATION

Key: Bovine 5' and 3' flanking (FL) sequences are blue; RAG-2 coding region is green & the interrupting neomycin gene is red. Note that the transcriptional orientation of the NEO gene is opposite to that of the RAG-2 gene.



The 4.5 Kb region containing the exons encoding the Mu constant region and associated transmembrane domain exons, were deleted and replaced with the loxP-flanked neomycin resistance cassette (Not I fragment)

Figure 3